

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/426,776

DATE: 02/05/2001
TIME: 13:26:05

Input Set : A:\es.txt
Output Set: N:\CRF3\02052001\I426776.raw

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3 <110> APPLICANT: DING, Jeak Ling
4 TAN, Nguan Soon
5 HO, Bow
6 LAM, Toong Jin
8 <120> TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ENCODING A SECRETORY SIGNAL FOR EXPRESSION AND
9 SECRETION OF HETEROLOGOUS RECOMBINANT PROTEINS
11 <130> FILE REFERENCE: 1781-0178P
13 <140> CURRENT APPLICATION NUMBER: US 09/426,776
14 <141> CURRENT FILING DATE: 1999-10-26
16 <160> NUMBER OF SEQ ID NOS: 22
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 29
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Chloramphenicol acetyltransferase (CAT) gene forward primer derived
27 from bacteria
29 <400> SEQUENCE: 1
30 gaagatctgc tggagaaaa aatcactgg 29
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 29
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Chloramphenicol acetyltransferase (CAT) gene forward primer derived
40 from bacteria
42 <400> SEQUENCE: 2
43 gcatcgccg tgccttaaaa aaattacgc 29
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 21
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial
51 <220> FEATURE:
52 <223> OTHER INFORMATION: OaVtgExon2 reverse primer derived from Oreochromis aureus vitellogenin
53 gene exon 2
55 <400> SEQUENCE: 3
56 ccaagttgga ctggcccccc a 21
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 19
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial
64 <220> FEATURE:
65 <223> OTHER INFORMATION: EGFP reverse primer derived from Aequoria victoria green fluorescent
66 protein
68 <400> SEQUENCE: 4
69 ccctcgccg acacgctga 19

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72 <210> SEQ ID NO: 5
73 <211> LENGTH: 29
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial
77 <220> FEATURE:
78 <223> OTHER INFORMATION: B-lactamase forward primer derived from bacteria
80 <400> SEQUENCE: 5
81 ccgggaccca gaaacgctgg tgaagtaa          29
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 29
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial
89 <220> FEATURE:
90 <223> OTHER INFORMATION: B-lactamase reverse primer derived from bacteria
92 <400> SEQUENCE: 6
93 gggcccggtta ccaatgctta atcagtgag          29
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 29
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Forward primer from BspSS
104 <400> SEQUENCE: 7
105 gggtcacgag ggtgcttgta ctacgtctt          29
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 30
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial
113 <220> FEATURE:
114 <223> OTHER INFORMATION: BamGal forward primer with BamHI restriction site and some beta-
115 galactosidase sequence derived from bacteria
117 <400> SEQUENCE: 8
118 ccatggatcc cgtgatttcg ttgccggtct          30
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 26
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: EagGal reverse primer with EagI restriction site
129 <400> SEQUENCE: 9
130 gcgacggccg ggcagacatg gcctgc          26
133 <210> SEQ ID NO: 10
134 <211> LENGTH: 21
135 <212> TYPE: PRT
136 <213> ORGANISM: Oreochochromis aureus
138 <400> SEQUENCE: 10
140 Met Arg Val Leu Val Leu Ala Leu Ala Val Ala Leu Ala Val Gly Asp
141 1          5          10          15
143 Gly Ser Asn Leu Gly

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147 <210> SEQ ID NO: 11
148 <211> LENGTH: 80
149 <212> TYPE: DNA
150 <213> ORGANISM: Oreochromis aureus
152 <400> SEQUENCE: 11
153 attcaacatc acagagcatg aggtgcttg tactagctct tctctggct ctcacagtgg 60
155 gggaccagtc caacttggg 80
158 <210> SEQ ID NO: 12
159 <211> LENGTH: 204
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Junction of Vtgss (derived from Oreochromis aureus) and CrFCES
165 (Carcinoscorpius rotundicauda ES - EcoRI-SalI flanking fragment of
166 Factor C) determined by sequencing using the Ac5 forward primer and
167 pcDNA3.1/BGH reverse primer
169 <400> SEQUENCE: 12
170 gtggaattct gcagatgcta ccggactcag atcaattcac atccaccagc catgagggtg 60
172 cttgtactag ctcttgctgt ggtctcgca gtgggggacc agtccaaatt gggggatcta 120
174 ggtctgtgtg atgaacgag gttegagtgt aagtgtggcg atccaggcta tgtgttcaac 180
176 attccagtga aacaatgtac atac 204
179 <210> SEQ ID NO: 13
180 <211> LENGTH: 51
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial
184 <220> FEATURE:
185 <223> OTHER INFORMATION: VtgCrFCES protein - Vtg derived from Oreochromis aureus and CrFCES
186 derived from Carcinoscopus rotundicauda ES - EcoRI-SalI flanking
187 fragment of Factor C
189 <400> SEQUENCE: 13
191 Met Arg Val Leu Val Leu Ala Leu Ala Val Ala Leu Ala Val Gly Asp
192 1 5 10 15
194 Gln Ser Asn Leu Gly Asp Leu Gly Leu Cys Asp Glu Thr Arg Phe Glu
195 20 25 30
197 Cys Lys Cys Gly Asp Pro Gly Tyr Val Phe Asn Ile Pro Val Lys Gln
198 35 40 45
200 Cys Tyr Phe
201 50
204 <210> SEQ ID NO: 14
205 <211> LENGTH: 152
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Part of the Vtgss-CAT (Vtgss from Oreochromis aureus - CAT of bacterial
211 origin) fusion in the pBSVtgCAT vector
213 <400> SEQUENCE: 14
214 atcgataagc ttgatgctac cggactcaga tcaattcaca tccaccagcc atgaggggtgc 60
216 ttgtactagc tcttgctgtg gctctgcag tgggggacca gtccaacttg ggggatctgc 120

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218 tggagaaaaa aatcactgga tataaccacg tt                               152
221 <210> SEQ ID NO: 15
222 <211> LENGTH: 59
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Part of the Vtgss-CAT (Vtgss from Oreochromis aureus - CAT of bacterial
228      origin) fusion in the pBSVtgCAT vector
230 <400> SEQUENCE: 15
231 ggcggggcggt aattttttta aggcacggcc gatgcgacgg tatcgataac ttgatatcg           59
234 <210> SEQ ID NO: 16
235 <211> LENGTH: 34
236 <212> TYPE: PRT
237 <213> ORGANISM: Artificial
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Part of the Vtgss-CAT (Vtgss from Oreochromis aureus - CAT of bacterial
241      origin) fusion in the pBSVtgCAT vector
243 <400> SEQUENCE: 16
245 Met Arg Val Leu Val Leu Ala Leu Ala Val Ala Leu Ala Val Gly Asp
246 1          5          10          15
248 Gln Ser Asn Leu Gly Asp Leu Leu Gln Lys Lys Val Thr Gly Trp Thr
249          20          25          30
251 Thr Val
254 <210> SEQ ID NO: 17
255 <211> LENGTH: 3
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Part of the Vtgss-CAT (Vtgss from Oreochromis aureus - CAT of bacterial
261      origin) fusion in the pBSVtgCAT vector
263 <400> SEQUENCE: 17
265 Gly Gly Ala
266 1
269 <210> SEQ ID NO: 18
270 <211> LENGTH: 66
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Part of the nucleotide sequence adjoining Vtgss (derived from Oreochromis
276      aureus) and CAT (derived from bacteria) in the vector psp-VtgCAT
278 <400> SEQUENCE: 18
279 ggcggggcggt aattttttta aggcacggcc gatgcgacgg tatcgatatt gttacaacac           60
281 cccaac                                           66
284 <210> SEQ ID NO: 19
285 <211> LENGTH: 155
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Nucleotide sequence of the Vtg-EGFP (Vtg derived from Oreochromis

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291 aureus - EGFP derived from Aequoria victoria) fusion in the vector
292 pVtgEGFP
294 <400> SEQUENCE: 19
295 gctagcgcta ccggactcag atcaattcac atccaccagc catgaggggtg cttgtactag      60
297 ctcttgctgt ggctctcgca gtgggggacc agtccaactt gggggatcca ccggtcgcca      120
299 ccatggtgag caagggcggtg gtgcagaact ccggg      155
302 <210> SEQ ID NO: 20
303 <211> LENGTH: 38
304 <212> TYPE: PRT
305 <213> ORGANISM: Artificial
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Amino acid sequence of the Vtg-EGFP (Vtg derived from Oreochromis
309 aureus - EGFP derived from Aequoria victoria) fusion in the vector
310 pVtgEGFP
312 <400> SEQUENCE: 20
314 Met Arg Val Leu Val Leu Ala Leu Ala Val Ala Leu Ala Val Gly Asp
315 1 5 10 15
317 Gln Ser Asn Leu Gly Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly
318 20 25 30
320 Val Val Gln Asn Ser Gly
321 35
324 <210> SEQ ID NO: 21
325 <211> LENGTH: 204
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Nucleotide sequence at the junction of Vtgss (derived from Oreochromis
331 aureus) and B-lactamase (derived from bacteria) in pBADVtgblactKana
333 <400> SEQUENCE: 21
334 ctctactgtt tctccatacc cgtttttttg ggctaacagg aggaattaac catgaggggtg      60
336 cttgtactag ctcttgctgt ggctctcgca gtgggggacc agtccaactt gggggatcca      120
338 gaaacgctgg tgaaagtaaa agatgctgaa gatcagtttg gtgcacgagt gggttacatc      180
340 gaactggatc tcaacagcgg taag      204
343 <210> SEQ ID NO: 22
344 <211> LENGTH: 51
345 <212> TYPE: PRT
346 <213> ORGANISM: Artificial
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Amino acid sequence at the junction of Vtgss (derived from Oreochromis
350 aureus) and B-lactamase (derived from bacteria) in pBADVtgblactKana
352 <400> SEQUENCE: 22
354 Met Arg Val Leu Val Leu Ala Leu Ala Val Ala Leu Ala Val Gly Asp
355 1 5 10 15
357 Gln Ser Asn Leu Gly Asp Pro Glu Thr Leu Val Lys Val Lys Asp Ala
358 20 25 30
360 Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn
361 35 40 45
363 Ser Gly Lys
364 50

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VERIFICATION SUMMARY
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Input Set : A:\es.txt
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